

## RAW SEQUENCE LISTING ERROR REPORT

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BIOTE

**BRANCH** 

Application Serial Number:	09/446,089	B
Source:	/638	
Date Processed by STIC:	4-17-01	

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.
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- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,
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FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216. PATENTIN 2.1 c-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax) PATENTIN 3.0 c-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE <u>CHECKER</u> <u>VERSION 3.0 PROGRAM</u>, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

## **Checker Version 3.0**

The Checker Version 3.0 application is a state-of the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address: http://www.uspto.gov/web/offices/pac/checker

1638

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/446,089B

DATE: 04/17/2001 TIME: 13:33:07

401

449

Does Not Comply Corrected Diskette Needed Input Set : A:\001560-377.ST25.txt Output Set: N:\CRF3\04172001\I446089B.raw see p.6 3 <110> APPLICANT: SAKAKIBARA, Keiko FUKUI, Yuko 5 TANAKA, Yoshikazu KUSUMI, Takaaki 6 MIZUTANI, Masako 8 NAKAYAMA, Toru 10 <120> TITLE OF INVENTION: GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY 12 <130> FILE REFERENCE: 001560-377 14 <140> CURRENT APPLICATION NUMBER: US 09/446,089B 15 <141> CURRENT FILING DATE: 1999-12-17 17 <150> PRIOR APPLICATION NUMBER: PCT/JP99/02045 18 <151> PRIOR FILING DATE: 1999-04-16 20 <150> PRIOR APPLICATION NUMBER: JP 10/107296 21 <151> PRIOR FILING DATE: 1998-04-17 23 <160> NUMBER OF SEQ ID NOS: 15 25 <170> SOFTWARE: PatentIn version 3.0 28 <210> SEQ ID NO: 1 29 <211> LENGTH: 1951 30 <212> TYPE: DNA 31 <213> ORGANISM: Antirrhinum majus 33 <220> FEATURE: 34 <221> NAME/KEY: CDS 35 <222> LOCATION: (96)..(1781) 37 <400> SEQUENCE: 1 38 aaattacatt getteetttg teecacette caccaccaat atatacaact teeteageta 60 40 gttgtttatt atcaatcaaa taaaattatt teeca atg tte aaa aat eet aat 113 Met Phe Lys Asn Pro Asn 41 161 44 atc ege tat cac aaa cta tet tee aaa tee aat gac aac gat caa gaa 45 Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu 10 15 48 tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc 209 49 Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe 30 35 257 52 cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg 53 Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg 40 45 50 56 ttt gee teg ace tea ace gge eet ate gee gee eet gat gte ace aaa 305 57 Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys 70 58 55 65 60 60 tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt 353 61 Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys 80 75

64 ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc

65 Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser

68 act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac

95

90

66



RAW SEQUENCE LISTING DATE: 04/17/2001 PATENT APPLICATION: US/09/446,089B TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

69 Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr 70 105 110 115 72 att goc aaa tto aag aaa goc gtt gag ctt atg cga gct cta cct gag 497 73 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu 125 130 130 76 gat gac cct cgt agc ttc aag caa caa gct act gct cat tgc gct tac 77 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr 81 135 140 145 150 80 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa 81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln 82 155 160 84 atc cac cga tct tgg ctt ttt ccg ttc cat aga tat tat act ac 85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr 86 170 175 180 88 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct 89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala 90 185 190 91 185 190 92 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca act cca tca 93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94 200 205 210 96 atg ttt att gat act act tct cg ctg tac gat agt tta cgg gac agt 97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 98 215 220 225 230 100 aat cat cag cca cca acc act gta gac ttg aca tac cct tcg at 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp 102 235 240 245 104 tcc gac aat acc act act cct gaa gag caa atg act acc act aca 105 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys 106 255 270 113 Phe Gly Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe 110 265 270 113 Phe Gly Arg Glo Cac acc act ggc atg act act act act acg ggt ttc 116 28 act act act act acg gga aca act ggg ggc act act act act acg gct ttc 117 Ser Ile Glu Leu Val Pro His Gly Met Ille His Leu Trp Thr Gly Ser 118 296 300 300 300 300 300 300 300 300 300 30																		
73 Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu 74 120 125 130 75 gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tge gct tac 77 Asp Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr 78 135 140 145 150 80 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa 81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln 82 155 160 165 84 atc cac cga tct tgg ctt ttt tcc cg ttc cat aga tat tat act tac 85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr 86 170 175 185 190 195 88 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct 89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala 90 185 190 195 92 ctc caa ttt tgg act at gat tca cct ggt gga atg aca act cca tca 93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94 200 205 210 94 200 205 210 96 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt 97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 98 215 220 225 230 100 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp 102 225 240 245 104 tcc gac aat acc act act cct gaa gag caa atg att ata acc ctt aaa 105 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys 106 250 250 260 108 att gtg tac aga caa atg gtg gac gac get aag act cca cag ctt tc 109 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Glu Leu Phe 110 265 270 112 ttc ggc cgc cca tac cga cgt gag aca agt tt cac ggg ggg gg 977 112 ttc ggc cgc cca tac gac gg gag caa gat tt cac ggg gg gg 977 112 ttc ggc cgc cca tac gac gg gag caa gat tt cac ggg gg gg 977 112 Glu Asn Thr Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 114 280 285 290 115 Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Glu Leu Phe 120 265 270 121 Glu Asn Thr Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 124 280 285 290 125 Arg Asp Pro Tir Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 126 Arg ag aac acg cct tat ggc gag aac atg gag gct ttc tac tca acg gct 127 Arg Arg P		Thr	Thr		Arg	Val	Arg	Arg		Ala	His	Leu	Val	_	Asp	Ala	Tyr	
120	72	att.	acc	aaa	ttc	aaq	aaa	acc	at.t.	σασ	ct.t.	at.o	cga	act	cta	cct	gag	497
74         120         125         130         76         gat gac cct cgt agc ttc aag caa gac aca gat cat tgc gct tac         545         77         Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr         78         135         140         145         150         150         181         181         Cys Ala Tyr         78         181         Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln         593         81         Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln         641         641         85         11e His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr         170         175         180         641<			_			_		-	-			_	_					
76 gat gac cct cgt age tte aag caa caa get aac gte cat tge get tae 77 Asp Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr 8 135 80 tge gog ggg geg tat aat caa gee ggt tte aca aac cta aag cte caa 11 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln 82 155 84 atc cac cga tet tgg ctt ttt tee cgt tee cat aga tat tat atc tae 85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ill Tyr 86 170 175 180 88 ttt ttt gaa aga ata tg gga aaa cta atc aat gat aca act tt get 89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala 90 185 190 195 92 ctc caa ttt tgg act tat gat tca cet ggt gga atg aca act cca tca 93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94 200 205 96 atg ttt att gat act act tet get gga atg agt tta cgg gac agt 97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 88 215 220 225 220 100 aat cat cag cca cca acc acc acc acc acc acc acc		110		1175	1 110	цуБ	<u>гу</u> 5		Val	OLU	Lica	IIC C	_	mru	пси	110	OIU	
77 Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr 78 135 140 145 145 150 1450 1450 1450 1450 14																		E 4 E
18		_	-		_	_		_			_		-		_	-		545
80 tgc gcg ggg gcg tat aat caa gcc ggt ttc aca ac cta aag ctc caa 81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln 82		-	Asp	Pro	Arg	Ser	Phe	Lys	Gln	Gln	Ala	Asn	Val	His	Cys	Ala		
81 Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln 82	78	135					140					145					150	
82	80	tgc	geg	ggg	gcg	tat	aat	caa	gcc	ggt	ttc	aca	aac	cta	aag	ctc	caa	593
82	81	Cys	Ala	Gly	Ala	Tyr	Asn	Gln	Ala	Gly	Phe	Thr	Asn	Leu	Lys	Leu	Gln	
84 atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac 85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr 86		-		_		_				_					-			
85 Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr 170	84	atc	cac	cga	tct		ctt	+++	ttc	cca		cat	aga	tat	tat		tac	641
86				-						_			-					0 2
88 ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct 89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala 90 185 190 195 92 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca 737 33 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94 200 210 96 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt 785 97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 98 215 220 225 230 100 aat cat cag cca acc acc atc gta gac ttg aac tac gcc ttt tct gat 833 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp 240 205 250 240 104 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa 881 105 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys 260 108 att gtg tac aga atg gtg tcg agc gct aag act cac acc acc act ggc ggt ggg 97 113 Phe Gly Arg Pro Tyr Arg Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe 265 116 tcg gec gcc ca tac cga cgt ggg gac aag act cac aca ggc ttt cac gac gat gtg tcg agc gtg aag act cac acg ggt ggg 97 113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 14 14 280 285 15 280 16 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct 1025 17 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser 11 18 295 300 19 305 10 30		116	III	Arg		ттЬ	пец	rne	FIIE		riie	птъ	Arg	TYL	_	116	TYL	
89 Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala 90																		600
90				-	-		_						_					689
92 ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca 737  33 Leu G1n Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94 200 205 210  96 atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt 785  97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 98 215 220 225 230  100 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp 102 235 240 245  104 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa 105 Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys 106 250 255 260  108 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc 109 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe 110 265 270 275  112 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg 113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 114 280 285 290  116 tcg att gag tta gtc ccc cat ggc atg ata cat tta tgg acc ggt tct 118 295 300 30 310  120 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct tot 121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 122 30 30 325  124 gag gac ccg ata ttt tt gct cat cat ccg agg acg gac gac gat gat aga atg tgg 1121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 122 325 320 325  124 gag gac ccg ata ttt tt gct cat cat ccg acg gac gac gac gat acc acc gac gac gac gac gac gac gac gac		Phe	Phe	Glu	Arg	Ile	Leu	GLY		Leu	Ile	Asn	Asp		Thr	Phe	Ala	
93 Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser 94	90			185					190					195				
94	92	ctc	caa	ttt	tgg	aac	tat	gat	tca	cct	ggt	gga	atg	aca	atc	cca	tca	737
94	93	Leu	Gln	Phe	Trp	Asn	Tyr	Asp	Ser	Pro	Gly	Gly	Met	Thr	Ile	Pro	Ser	
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97 Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser 98 215		atσ		att	gat	act	aat		tca	cta	tac	gat		tta	caa	gac	agt	785
98 215		_			_				_	_		-	_			-	_	700
100 aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat 833 101 Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp 245 104 tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa 881 105 Ser Asp Asn Thr Thr Thr Pro Glu Gln Met Ile Ile Asn Leu Lys 265 106			FIIC	TTE	ASP	TIIT		261	Ser	цец	тАт		Ser	пеа	ALG	ASD		
101 Asn His Gln Pro																		
102   102   235   240   245   245   245   245   245   246																		833
104 tcc gac aat acc act act cct gaa gag caa atg atg atg atg atg atg atg atg atg a			His	Gln	Pro			Ile	· Val	. Asp			туг	: Ala	Phe	e Ser	Asp	
105   Ser   Asp   Asn   Thr   Thr   Thr   Pro   Glu	102	?				235	5				240	)				245		
106	104	tcc	gac	aat	acc	act	act	. cct	gaa	gag	, caa	atg	, att	: ata	aac	ctt	aaa	881
108 att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc 929 109 Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe 110	1.05	Ser	Asp	Asn	Thr	Thr	Thr	Pro	Glu	Glu	ı Gln	Met	: I1e	e Ile	Asn	Leu	Lys	
109   The Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe	106	i			250	)				255	;				260	)		
109   The Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe	108	att	ata	tac	ада	саа	ato	ata	tca	agr	e act	. aao	ract	. cca	сао	r att	ttc	929
110																		
112 ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg 977  113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 114 280			, , ,	-	_	0111		· · ·										
113 Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly 114								~~+								. ~+~	~~~	077
114																		9//
116 tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct 117 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser 118 295					Pro	ıyr	· Arg			Asp	Gin	1 GIU			) GIĀ	va <sub>1</sub>	GTA	
117 Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser 310  120 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct 1073  121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala  122																		
118 295	116	tcg	att	gag	tta	gtc	cct	cat	ggc	. atg	r ata	cat	. tta	ı tgg	acc	ggt	tct	1025
120 gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct 1073 121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 122	117	Ser	Ile	Glu	Leu	Val	Pro	His	Gly	Met	Ile	His His	Leu	ı Trp	Thr	· Gly	Ser	
121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 122	118	295					300					305					310	
121 Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala 122	120	qaq	aac	acq	aaa	tat	ggc	qaq	aac	atq	dad	get	ttc	: tac	tca	acq	gct	1073
122																		
124 aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg 1121 125 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp 126						-	_		220					1 -	20			
125 Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp 126			~~~	000	2+2			aat	an t	an t			a+c	. ~=+	200			1121
126 330 335 340  128 toc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat 1169  129 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp  130 345 350 355																		1121
128 tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat 129 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp 130 345 350 355		_	ASP	Pro			Pne	Ald	HIS			ASII	val	. ASD	_		ттр	
129 Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp 130 345 350 355																		
130 345 350 355																		1169
			Ile		Lys	Thr	Leu	${ t Gly}$			Arg	Arg	Thr			Thr	Asp	
132 one get tot get geg tot the get tot the get tet tet geg gee eeg gee geg geg	130			345					350					355				
132 cca gat tet cet gat geg tet tet get tet tat gat gat dat ged gag 1217	132	cca	gat	ttt	ctt	gat	gcg	tct	ttc	gtt	ttt	tat	gac	gaa	aac	gca	gag	1217
133 Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu	132	Pro	Asp	Phe	Leu	Asp	Ala	Ser	Phe	Va1	Phe	Tyr	Asp	Glu	Asn	Ala	Glu	



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/446,089B

DATE: 04/17/2001 TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

134		360					365					370					
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138	375					380					385					390	
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141	Tyr	Val	Tyr	Gln	Asp	Val.	Glu	Ile	Pro	Trp	Leu	Asn	Thr	Arg	Pro	Thr	
142					395					400					405		
144	cca	aaa	gtt	tct	ccg	tct	cta	ctt	aag	aaa	ttt	cat	aga	aca	aac	act	1361
145	Pro	Lys	Val	Ser	Pro	Ser	Leu	Leu	Lys	Lys	Phe	His	Arg	Thr	Asn	Thr	
146		_		410					415					420			
148	gcc	aat	ccg	aga	caa	gtt	ttt	cct	gcg	ata	ctt	gac	aga	gtc	tta	aaa	1409
149	Āla	Asn	Pro	Arg	Gln	Val	Phe	Pro	Ala	Ile	Leu	Asp	Arg	Val	Leu	Lys	
150			425	_				430					435				
152	gtt	atc	gtg	acq	agg	ccg	aag	aaa	act	aga	agt	agg	aaa	gaa	aag	gac	1457
	Val																
154		440			_		445					450					
156	gag	tta	gaa	gag	att	tta	gtg	att	gaa	ggg	att	gaa	ctg	gaa	aga	gac	1505
157	Glu	Leu	Glu	Glu	Ile	Leu	Val	Ile	Glu	Gly	Ile	Glu	Leu	Ğlu	Arg	Asp	
158	455					460				-	465				_	470	
160	cac	aaa	cac	qta	aaa	ttc	qac	gtt	tat	att	aat	gct	gac	gaa	gat	gac	1553
	His			_				_				-		-			
162		-			475		-		-	480			•		485	_	
164	ctt	gcg	gtg	att	tcg	ccg	gag	aat	gct	gag	ttc	gcc	ggq	agt	ttc	gtg	1601
	Leu				_	-			_			_		_			
166				490					495				_	500			
168	agt	ctq	tgg	cac	aaa	cct	ata	aag	ggg	aag	agg	aca	aaq	acg	cag	tta	1649
169	Ser	Leu	Trp	His	Lys	Pro	Ile	Lys	Gly	Lys	Arg	Thr	Lys	Thr	Gln	Leu	
170			505		_			510					515				
172	tta	aca	ttg	tcg	att	tgt	gat	att	ttg	gag	gat	ttg	gat	gct	gac	gaa	1697
173	Leu	Thr	Leu	Ser	Ile	Cys	Asp	Ile	Leu	Glu	Asp	Leu	Asp	Ala	Asp	Glu	
174		520					525					530					
176	gat	gat	tat	gtg	ttg	gtc	act	ttg	gtt	ccg	aga	aac	gcc	gga	gat	gcg	1745
	Asp																
178	535	_				540					545				_	550	
180	atc	aag	att	cat	aat	gtc	aag	att	gag	ctt	gat	ggc'	taat	aaat	tc		1791
181	Ile	Lys	Ile	His	Asn	Val	Lys	Ile	Glu	Leu	Asp	Gly					
182		ŧ			555		_			560	_	-					
184	tatt	gatt	tc t	tctc	caaco	ct ac	agtt	gato	att	taco	gat	tgat	tatt	cc a	aataa	aagta	1851
		-					_	-			_	_				ttaaa	1911
188	agca	agtto	ıta t	aaat	ggto	ja aa	taac	gatt	: act	tttt	gag	_					1951
191	<210	)> SE	EQ II	NO:	2		_										
192	<211	L> LE	NGTE	I: 56	2												
193	<212	?> TY	PE:	PRT													
194	<213	3> OF	RGANI	SM:	Anti	rrhi	num	maju	ıs								
196	<400	)> SE	QUEN	ICE:	2												
198	Met	Phe	Lys	Asn	Pro	Asn	Ile	Arg	Tyr	His	Lys	Leu	Ser	Ser	Lys	Ser	
199	1				5			-		10					15		
202	Asn	Asp	Asn	Asp	Gln	Glu	Ser	Ser	His	Arg	Cys	Lys	His	Ile	Leu	Leu	
203				20					25					30			



RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/446,089B

DATE: 04/17/2001 TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

Output 560. N. (ONE 5 (041/2001) 14400055.14W

	Phe	Ile		Thr	Leu	Phe	Leu		Ile	Val	Gly	Leu		Ile	Ala	Asn
207			35					40				_,	45	_		
	Ser		Ala	Tyr	Ala	Arg		Ala	Ser	Thr	Ser		GLY	Pro	ITe	Ala
211		50	<b>3</b>	**- 7	m1	<b>T</b>	55	<b>a</b> 1	a1	D	<b>3</b>	60	D	D	<i>α</i> 1	m la sa
	Ala	Pro	Asp	va⊥	Thr	_	Cys	GTĀ	GIn	Pro		ьeu	Pro	Pro	GIY	
	65	D	т1 а	70 ~~ ~~	Q== =	70	D	Dece	т1.	Dana	75	T *** 61	т1.	т1.	7 ~~	80 Dha
219	Ala	PIO	тте	ASII	85	Cys	Pro	PIO	тте	90	Ald	цув	тте	TIE	95	Pile
	Glu	Lou	Pro	Dro		Cor	Thr	Thr	Ma+		17 a 1	λησ	Δνα	Δla		ніс
223		пец	FIO	100	FIO	Ser	7.11.1	1111	105	Arg	Val	Arg	AL 9	110	AIu	1112
	Leu	Val	Asp		Δla	Tur	T1e	Δla		Phe	Lvs	Lvs	Ala		Glu	Leu
227		,	115			-1-		120	-4-			-2 -	125			
230	Met	Arg	Ala	Leu	Pro	G1u	Asp		Pro	Arq	Ser	Phe	Lys	Gln	Gln	Ala
231		130					135	-		_		140	_			
234	Asn	Val	His	Cys	Ala	Tyr	Cys	Ala	Gly	Ala	Tyr	Asn	Gln	Ala	Gly	Phe
235	145					150					155					160
238	Thr	Asn	Leu	Lys	Leu	G1n	Ile	His	Arg	Ser	Trp	Leu	Phe	Phe	Pro	Phe
239					165					170					175	
	His	Arg	Tyr	-	Ile	${ t Tyr}$	Phe	Phe		Arg	Ile	Leu	Gly		Leu	Ile
243			_	180		_			185					190	_	
	Asn	Asp		Thr	Phe	Ala	Leu		Phe	Trp	Asn	Tyr	_	Ser	Pro	GTA
247			195	m 1	_	~		200	<b>~1</b> .		<b>m</b> 1	3	205	<b>a</b>	т	m
	Gly		Thr	шe	Pro	ser		Pne	TTE	Asp	Thr		ser	ser	Leu	ryr
251	7 ~~	210	T 011	71	7.00	Con	215	IIi a	Cln	Dwo	Dro	220	T 1 🛆	1701	7 an	T OU
	Asp 225	per	Leu	Arg	Asp	230	ASII	птр	GIII	PTO	235	1111	TTE	Val	ASP	240
	Asn	Щ22.75	Δla	Dha	Ser		Ser	Agn	Δcn	Thr		Пhr	Pro	Ġlu	Glu	
259	ASH	- y -	пια	1.110	245	пор	per	пор	Abn	250	1111	1111	110	OIG	255	OIII
	Met	Ile	Ile	Asn		Lvs	Ile	Val	Tvr		Gln	Met	Val	Ser	Ser	Ala
263				260		2			265	- 3				270		
266	Lys	Thr	Pro	Gln	Leu	Phe	Phe	Gly	Arg	Pro	Tyr	Arg	Arg	Gly	Asp	Gln
267			275					280					285			
270	Glu	Phe	Pro	Gly	Val	Gly	Ser	Ile	Glu	Leu	Val	Pro	His	Gly	Met	Ile
271		290					295					300				
	His	Leu	${\tt Trp}$	Thr	Gly		Glu	Asn	Thr	Pro	_	Gly	Glu	Asn	Met	
	305				_	310					315					320
	Ala	Phe	Tyr	Ser		Ala	Arg	Asp	Pro		Phe	Phe	Ala	His		Ser
279		**- 1	3		325	m	<b>a</b>	T7 -	m	330	m 1	<b>T</b>	<b>a</b> 1	a1	335	3
282	Asn	val	Asp	arg	Met	тгр	ser	тте	345	гйг	rnr	ьeu	GTÀ	350	Pro	Arg
	Arg	Пhr	7 an		Thr	Nan	Dro	7 an		Lou	λan	7. T.a	Sor		17 ⊃ 1	Pho
287	Arg	TIIT	355	ьеα	TIIT	дар	FIU	360	FIIE	пец	авр	ALG	365	FIIC	Val	FIIC
	Tyr	Agn		Δgn	Δla	Glu	Met		Ara	Val	Lvs	Va1		Asn	Cvs	Leu
291	~ <i>J</i> ~.	370	<b>9</b>	11011	112.0	· · · ·	375	,	9		1-	380	5	e	0,2	
	Asp		Lys	Lys	Leu	Gly		Val	Tyr	Gln	Asp		Glu	Ile	Pro	Trp
	385		<b>4</b>	-4 ·-		390			-		395			-		400
	Leu	Asn	Thr	Arg	Pro	Thr	Pro	Lys	Val	Ser	Pro	Ser	Leu	Leu	Lys	Lys
299				-	405					410					415	
302	Phe	His	Arg	Thr	Asn	$\mathtt{Thr}$	Ala	Asn	Pro	Arg	Gln	Val	Phe	Pro	Ala	Ile

 RAW SEQUENCE LISTING
 DATE: 04/17/2001

 PATENT APPLICATION: US/09/446,089B
 TIME: 13:33:07

Input Set : A:\001560-377.ST25.txt

Output Set: N:\CRF3\04172001\I446089B.raw

```
303
                420
306 Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
                                                     445
         435
                                440
310 Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
311
                            455
314 Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
315 465
                        470
                                             475
318 Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
                    485
                                        490
322 Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
                                                         510
323
                500
                                    505
326 Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
327
          515
                                520
330 Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
                                                 540
                            535
331
       530
334 Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
335 545
                        550
                                             555
338 Asp Gly
342 <210> SEQ ID NO: 3
343 <211> LENGTH: 13
344 <212> TYPE: PRT
345 <213> ORGANISM: Antirrhinum majus
347 <400> SEQUENCE: 3
349 Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
350 1
352 <210> SEQ ID NO: 4
353 <211> LENGTH: 12
354 <212> TYPE: PRT
355 <213> ORGANISM: Antirrhinum majus
357 <400> SEQUENCE: 4
359 Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
360 1
362 <210> SEQ ID NO: 5
363 <211> LENGTH: 18
364 <212> TYPE: PRT
365 <213> ORGANISM: Antirrhinum majus
367 <400> SEQUENCE: 5
369 Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
370 1
                                        10
372 Glu Phe
375 <210> SEQ ID NO: 6
376 <211> LENGTH: 29
377 <212> TYPE: PRT
378 <213> ORGANISM: Antirrhinum majus
380 <220> FEATURE:
381 <221> NAME/KEY: UNSURE-
382 <222> LOCATION: (9)..(9)
383 <223> OTHER INFORMATION: Amino acid 9 is Xaa wherein Xaa = unknown or other.
385 <220> FEATURE:
```

See p. 6

```
Seg # 6
<210>
       6
<211>
       29
<212>
       PRT
<213>
       Antirrhinum majus
<220>
      UNSURE (9)..(9) -> Xaa is at position 8
<221>
<222>
       Amino acid 9 is Xaa wherein Xaa = unknown or other.
                         Xaa is at position 28
<220>
<221>
       UNSURE
       (29)..(29) ->
<222>
<223>
       Amino acid 29 is Xaa wherein Xaa = unknown or other.
<400>
Lys Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val Arg 1 5 10 15
Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys 20 25
```

F.4.1,

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/446,089B

DATE: 04/17/2001 TIME: 13:33:08

Input Set : A:\001560-377.ST25.txt
Output Set: N:\CRF3\04172001\I446089B.raw

L:392	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:6
L:395	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:6
L:441	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:8
L:456	M:341	w:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:9
L:481	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:11
L:496	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:12
L:511	M:341	W:	(46)	"n"	or	"Xaa"	used,	for	SEQ	ID#:13